

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning at page 11, line 5 with the following replacement paragraph:

2. Using any method known in the art, compare the potential targets to the appropriate genome database (human, mouse, rat, etc.) and eliminate from consideration any target sequences with significant homology to other coding sequences. One such method for such sequence homology searches is known as Basic Local Alignment Search Tool (BLAST), which is available at ~~www.ncbi.nlm.nih.gov/BLAST~~ the National Institutes of Health (NIH)/National Library of Medicine's (NLM's) National Center for Biotechnology Information (NCBI) website.

Please replace the paragraph beginning at page 11, line 11 with the following replacement paragraph:

3. Select one or more sequences that meet your criteria for evaluation. Further general information about the design and use of siRNA may be found in "The siRNA User Guide," available at ~~www.mpibpc.gwdg.de/abteilungen/100/105/sirna.html~~ the Max Planck Institute for Biophysical Chemistry website.